

IN THE SEQUENCE LISTING:

g Please delete the Sequence Listing of record, and replace same with the attached substitute Sequence Listing.

IN THE SPECIFICATION:

Please replace the paragraph beginning at page 24, line 13 with the following paragraph:

g2 --Figure 1 is a representation showing predicted amino acid sequences encoded by murine *bcl-w* cDNAs (top line, "Bcl-w", SEQ ID NO: 9) and chimaeric cDNAs corresponding to transcripts spliced from exon 3 of the *bcl-w* gene to an exon of the adjacent *rox* gene (bottom line, "Bcl-w-Rox", SEQ ID NO: 10). Boxes highlight the regions of highest homology within the Bcl-2 family, denoted S1, S2 and S3 (Cory, 1995). The arrowhead marks the position corresponding to an intron within the gene. Two residues that differ in human Bcl-w are indicated above the mouse sequence. Not all of the *rox* cDNA sequences was determined in both orientations.--

Please replace the paragraph beginning at page 26, line 20 with the following

paragraph:

g3 --Figure 8 is a representation of a comparison of survival and anti-survival Bcl-2 sub-families. Human Bcl-2 (SEQ ID NO: 11), Bcl-x_L (SEQ ID NO: 12), Bcl-w (SEQ ID NO: 7), Bax (SEQ ID NO: 13) and Bak (SEQ ID NO: 14) amino acid sequences were aligned by the Wisconsin PILEUP program. The most conserved portion of the Ced 9 sequence (SEQ ID NO: 15) and a short conserved segment in Bik are also shown. Gaps made in individual sequences to optimise alignment are indicated by dots. Residues identical or very similar (L ~ M; E ~ D; K ~ R; V ~ I) in the survival-promoting proteins Bcl-2, Bcl-x_L and Bcl-w are shown on a black background, as are also those identical or very similar in all the Bcl-2 homologues. A grey

93
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background indicates residues shared by Bak and Bax but not present in the survival proteins. Homology regions S1, S2 and S3 (Cory , 1995) and the hydrophobic C-terminal segment are boxed, while the BH1, BH2, BH3 and NH1 regions defined by others (Yin *et al.*, 1994; Subramanian *et al.*, 1995) are overlined. Filled arrowheads indicate conserved residues specific to the survival proteins; open arrowheads, those specific to anti-survival proteins. An unbroken arrow indicates the position of the splice site common to all the proteins; a broken arrow, the position of the alternative 5' splice that creates the smaller Bcl-x protein and a wavy line a conserved C-terminal motif.--

Please replace the paragraph beginning at page 27, line 6 with the following

94

paragraph:

--Figure 9 is a representation of the coding region of (A) human (SEQ ID NO: 6) and (B) murine (SEQ ID NO: 8) *bcl-w*--

REMARKS

In the Office Action dated July 1, 2002, Claims 21-24 are pending and are under consideration. The Examiner objects to the amendment filed on January 23, 2002 under 35 U.S.C. §132, alleging that the amendment introduces new matter into the disclosure. More specifically, the Examiner alleges that the newly submitted Sequence Listing is not supported by the specification as originally filed. The Examiner has also objected to the proposed drawing correction and the proposed substitute sheets of drawings, filed on January 23, 2002, allegedly because they introduce new matter into the drawings. More specifically, the Examiner alleges that the original disclosure does not support the changes made in the nucleotide/amino acid sequence of Figure 9A and 9B. Moreover, the Examiner has rejected claims 21-24 under 35 U.S.C. 112, first paragraph, as containing subject matter which is not described in the